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Best Local Similarity
Matches 2370; Conser
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GCTATGAAGGGTTTGTGACCACACACACTCTCCTGGCCCCCTGTCCTTTTGGAAAGAAGA 600
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                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 2383)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project Unpublished
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/db_xref="taxon:9606"
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99.8%; Pred. No. 0;
50; Mismatches 3;
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1621 CAGGAAACCATTTCCAAACTGCCAAGCCATGGCAGAGTATCAAGACCTCAGGAACCATCG 1680	8
1561 CTGGAAGGTTGAAGGGTTTGTTCCCAGTCACACAACCAGGGATCCTTAGGACAGCCAGAC 1620 	В б
1501 GGCCCCAGGGCCTCAGGAAACTTGCACCCCAACCCTCTCATTTTACAGAAGAAAACTGTGC 1560	p &
1441 CTTTATGAGTACTTCCATAGGAGGAGGAGACAGGGAGTGGGGGAGATAAACTCAGCCACAA 1500 	B 63
1381 GCTCCTGTGTGTGGGGGCTGGGGGACCTTGTGTGCCTTTTCCTTGTGGCTGTGAAATG 1440	B 8
1321 GAAGAACTTGCGTGTGCTGGGGGAGAGGAAGCCTGGCCTTGAGGGAGG	B 8
1261 GAGAAGCCATGGCTGGGCCGTTCCATTCTGGGGAGCTGCTGAAAAGAGCTGGGAGGCCGA 1320	<u>සි</u> . හි
1201 TCAAAGGAAAAATGTGCTCTACTCCACCCACTCCCAGCTCTGCCAAGAAGCTGTCCTCT 1260	B 5
1141 TCTCTCTGTGGGCTGTTGGGCCCCAGGGCAGCTGAAGAGGGTTGACAGCCCTTTGGACC 1200	유 성
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961 TGGCAGTGGGTCTGTTGATGAGAGAACTTTAAGGGCCCAATCAGTCCCTGGGCACCCCCT 1020 	용 <i>청</i>
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841 TCCACCCTTCCCCAGTTTAACCTTTGACAGGATCTTCACCTCTCTGATCAGCATTGC 900	B &
781 CGCTGTTTGGAAGAACAGGTGAGCGACGGTGGGGAATTTCAGAGGCCTGGGCCCACCGCC 840	용 성
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661 AACAAGAAGAAAAACCAAAAACCCACGAATGAAAACATTCCTTTCTCAGCTCAGATC 720	B 8
601 CAGGGATGAAATATAATCAAGCAATTAACCACCCCCATCATCACCAAGAACAACAGTATC 660	g 8
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	2341 TCAATAAATTACACATGCACTTACGTAAAACACA 2374 	2 2 2 3
2339	GATTCCCAGGAAGTCCAGCCCGAGCTGATTCACAGAACAAATGCATGC	
2340	ZZO ARGESTACIGETIGENERALES SANTENES PROPERES POR SENTENCIA PRESENTA LO LI LECLIO. LE CONTROLLO DE LA CONTROLLO) F
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2219		Db 2
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1920		Qy 1:
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1800	1741 AGTGTGCATGGAGCCCATGACTGCGGGGTTTTGTAGACACCTCAGGGATTACATGACTGG	ם ממ
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1740	1681 AGACACCATGGAAAGCATTGGGAAAAGCCTTCCTTAGCTTTTGAAGCTCCTCATTGTTCTTG	Db 1
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1680	1621 CAGGAAACCATTTCCAAACTGCCAAGCCATGGCAGAGTATCAAGACCTCAGGAACCATCG	Db 1

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ACAA	1064 CTTTATGAGTACTTCCATAGGAGGAGGAGCAGGAGGAGGAGATAAACTCAGCCA L501 GGCCCCAGGGGCCTCAGGAAACTTGCACCCAACCCTCTCATTTTACAGAAGAAAACTG 1511	Db 5
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S=S	.141 TCTCTCTCTGTGGCTGTTGGGCCCCAGGGCAGCTGAAGAGGGTTGACAGCCCTTTGGA 	Db 4:
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3=3	661 AACAAGAAGAACAGGGACAACAAAACCCACGGATGAAACATTCCTTTCTCAGCTCAGA?	4 9
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RESULT 3
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Sequence Moth Listing for SER ID NO:5

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US-09-385-982-202/c

Sequence 202, Application US/09385982

Patent No. 6262334

GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NUMBER: US/09/385,982

CURRENT PILING DATE: 1999-08-30

EARLIER PILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: 06/117,393

EARLIER APPLICATION NUMBER: 60/117,393

EARLIER APPLICATION NUMBER: 60/098,639

EARLIER PILING DATE: 1999-08-31

NUMBER: OF SEQ ID NOS: 544

SOPTWARE: PAST SEQ ID NOS: 544

SOPTWARE: PAST SEQ ID NOS: 544

SOPTWARE: PAST SEQ ID NOS: 544

SOPTWARE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

JOHER INFORMATION: n = A,T,C or G

US-09-385-982-202
                                                                                                                Query Match 0.8%; Score 18; DB 4; Length 620; Best Local Similarity 100.0%; Pred. No. 37; Matches 18; Conservative 0; Mismatches 0; Indels
                                                      628 ACCACCCCATCATCACC 645
349 ACCACCCCATCATCACC 332
                                                                                                                    0; Gaps
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Page 7

밁 밁 S 문 S 밁 S 片 S 뭉 S 묽 Ś 뭉 COMMENT Ş. á Ş 문 á δ ORIGIN FEATURES 밁 BASE COUNT Query Match Best Local Similarity Matches 2370; Conserv 48804 48744 CAAATATGTGTTTATTCCTGCGTGGGGCCACAGGCTGGTTTCTTGGGTGCAATGAAT 48803 48684 TATTTCTCAGGATGACCCTGCGAGACAGGCCAGGGTCATTAGACCCAATTTGGTTCTCAG 48743 48624 CTTTTCTCTTGAGTGCAAATGGAGAACAGCTGCTCACGCTCGTCGTCTGACACTCAGC 48683 49044 48924 48864 49104 48984 STS source 181 421 361 301 241 121 541 481 601 13 μ CACTCCGGACCCCGGAGAGTGAAGACTCTGCCTGTCGGACTTGCTTTGAGAAGATCCTTC 300 CAAATATGTGTTTATTCCTGCATGCGTGGGCCACAGGCTGGTTTCTTGGGTGCAATGAAT 180 CAGGGATGAAATATAATCAAGCAATTAACCACCCCCATCATCACCAAGAACAACAACAGTATC 660 TCCACCTCCCCATGGCAGAAGTTGCTTCACAGAGGGGAACAGTTTTATGGATGTGGCTGA 360 CACTCCGGACCCCGGAGAGTGAAGACTCTGCCTGTCGGACTTGCTTTGAGAAGATCCTTC TATTTCTCAGGATGACCCTGCGAGACAGGCCAGGGTCATTAGACCCAATTTGGTTCTCAG 120 GCTATGAAGGGTTTGTGACCACAGAGTCTCCTCGCCCCTGTCCTTTTGGAAAGAAGA 600 TTCCAAGAGGGTGTGGATTCCCTGCCATCCCCACATGGTCAAGTGGAGGGGACGGGAAAAA 540 CTTCACCTTGGATGTAGTGCTGTTTCTAGGATCTCTTTTCAATCAGCAAAACAGGGGATG CTTCACCTTGGATGTAGTGCTGTTTCTAGGATCTCTTTTCAATCAGCAAAACAGGGGATG 480 GCTATGAAGGGTTTGTGACCACACAGACTCTCCTGGCCCCCTGTCCTTTTGGAAAGAAGA 49223 TTCCAAGAGGGTGTGGATTCCCTGCCATCCCACATGGTCAAGTGGAGGGGACGGGAAAAA 49163 TCCACCTCCCCATGGCAGAAGTTGCTTCACAGAGGGGAACAGTTTTATGGATGTGGCTGA Japan Science and Technology Corporation (JST) 5-3, Yonbancyo, Chiyoda-Ku, Tokyo, 102-0081 Japan For further infomation about this sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp. Tel:81-3-5214-8491, Fax:81-3-5214-8470)
This sequence is conducted by Japanese Foundation for Research as a JST sequencing Team.
Principal Investigator: Yusuke Nakamura Ph.D Phone:+81-3-5449-5372, Fax:+81-3-5449-5433, Yusuke@hgc.ims.u-tokyo.ac.jp
The sequence is submitted by Human Genome Sequencing project of JST TTCTCTTGTTGAGTGCAAATGGAGAACAGCTGCTCACGCTCGTCGTCTGACATCAGC 60 24961 a Conservative /standard_name="D8S571"
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a 22749 c 24235 g 28036 t /map="8p11.2" 66183. .66318 Location/Qualifiers db_xref="taxon:9606" organism="Homo sapiens" 99.2%; .66318 0; Mismatches Score 2356.6; Pred. No. 0; DB is between each flanking site 4 9; 19 Indels Length 100000; for Cancer 1; ä ALIS Gaps 49103 48983 48923 49043 ۲,

Homo sapiens genomic DNA, region, section 3/19.
AP000067
AP000067.1 GI:4579988 AP000067 NA, chromosome DNA 1i me 8p11.2, linear inear PRI senescence 25-MAY-2002 gene

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April 8, 1999

review history on page 3)

ACCESSION VERSION KEYWORDS

RESULT 4 AP000067 LOCUS

DEFINITION

Homo sapiens Homo sapiens DNA.

SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Isomura, M., Ikegawa, S., Kinjo, T. and Nakamura, Y.
DNA sequence analysis of a 1.9-Mb region on chromosome
Published Only in Database (1999)
2 (Dases I to 10000)
Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
Direct Submission 8p11.2

TITLE JOURNAL REFERENCE REFERENCE AUTHORS

AUTHORS TITLE

Submitted (12-FEB-1999) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Database Department; 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp,